

Gencore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 ; Search time 1441.15 Seconds  
(without alignments) 15778.007 Million cell updates/sec

Title: US-09-497-967-5  
Perfect score: 1404  
Sequence: 1 atgaaacaatccatctgtt.....tgatctttactacacctgtg 1404

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : EST:  
 1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estcom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_liv:\*

20: em\_gss\_pnt:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fan:\*

23: em\_gss\_man:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rnd:\*

## ALIGNMENTS

RESULT 1  
BQ134889/c  
LOCUS BQ134889 DEFINITION INITI1-D07.bl\_A006 G5 trophot mRNA linear EST 22-APR-2002  
multifiliis cDNA, mRNA sequence.  
ACCESSION BQ134889  
VERSION BQ134889.1  
KEYWORDS EST  
SOURCE  
ORGANISM Ichthyophthirius multifiliis  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Ophryogenina; Ichthyophthirius.  
REFERENCE 1 (bases 1 to 502)  
AUTHORS Clark, T., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,  
Dickerson, H., Lin, T.-L. and Pratt, L.H.  
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: umpratt@uga.edu  
Sequences have been trimmed to exclude polyA, vector, and regions  
below Phred quality 16. The threshold for highest quality sequence  
is 20.  
Seq primer: JEN REV  
High quality sequence stop: 474

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	54.4	3.9	502	14 BQ134889	BQ134889 INITI1_1-D
C 2	54.4	3.9	590	14 BQ135179	BQ135179 INITI1_4-C
C 3	54.4	3.9	602	14 BQ135164	BQ135164 INITI1_4-B
C 4	54.4	3.9	607	14 BQ134912	BQ134912 INITI1_1-F
C 5	54.4	3.9	658	14 BQ135057	BQ135057 INITI1_2-G
C 6	51.2	3.6	445	14 BQ134871	BQ134871 INITI1_1-B

FEATURES	POLYA=Yes. Location/Qualifiers	FEATURES	source	Location/Qualifiers
source	1. .502 /organism="Ichthyophthirius multifiliis" /strain="G5"	1. .590 /organism="Ichthyophthirius multifiliis"		
	/db_xref="taxon:5932"	/strain="G5"		
	/clone.lib="G5 trophont cDNA (INIT1)"	/clone.lib="G5 trophont cDNA (INIT1)"		
	/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >200 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."	/note="Vector: pBluescript SK(-) from Lambda Zap II; Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >200 bp cloned into lambda ZAP II. Plasmid DNA for sequencing was prepared by mass excision."		
BASE COUNT	185 a 80 c 70 9 167 t	BASE COUNT	207 a 103 c 94 g 186 t	
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	Query Match 3.9%; Score 54.4; DB 14; Length 502; Best Local Similarity 51.7%; Pred. No. 0.00072; Matches 155; Conservative 0; Mismatches 136; Indels 9; Gaps 1;	Query Match 3.9%; Score 54.4; DB 14; Length 590; Best Local Similarity 51.7%; Pred. No. 0.00079; Matches 155; Conservative 0; Mismatches 136; Indels 9; Gaps 1;		
	QY 1114 CCTACCTGTATGGCTAGTGGCTGTCGACTGGACTGCTGAACTGGTGACCGAACGGTGGAA 1173	QY 1114 GCTACCCUGATCGCTCACTGCTGAGCTGGTGAACCCGACCGGA 1173		
	Db 379 GTACTTCAGGCCACATAATGTTAACGATTGGCCCTGCCTGAGTGTATGATGT 320	Db 373 GCTACTTCAGCCACATAATGTTAACGATTGGCCCTGCCTGAGTGTATGATGT 314		
	QY 1174 ACCACCTCTACCTACAAAGCAGGTGCTAGTGGTAACTTCTAC 1233	QY 1174 ACCACCTCTACCTACAAAGCAGGTGCTAGTGGTAACTTCTAC 1233		
	Db 319 AGATCAAATTAATTGGTAGCTTAGAAGTGTAACTAAATGTTAGGCTTAACTTTAT 260	Db 313 ACATCAACTAAATTGGTAGCTTAAAGTGTAACTAAATGTTAGGCTTAACTTTAT 254		
	QY 1234 ACCACCAAGCAGACCGACTGGGTGGCTGGAAATCGACACCCTGTAACAGAG 1293	QY 1234 ACCACCAAAGCAGACCGACTGGGTGGCTGGAAATGCAACTCTGTAAACAGAG 1293		
	Db 259 GCATCAAAACATCTGGTTTGACGGAGTAACTGATACTGAAATGTCATAAAA 200	Db 253 GCATCAAAACATCTGGTTTGAGCAGGTAACTGATACTGAAATGTCATAAAA 194		
	Qy 1294 CTCACCTGTGAGCTGCTGGCTGCTGAGTCTGCTAAAGAAACATCACAGTGAC 1353	QY 1294 CTGACCTCTGGAGCTGAGSGCTAACCTGGCTGAGTCTGCTAAAGAAACATCCAGTGAC 1353		
	Db 199 TTAACTCTGTGCTAGCTAACGTTAAAGTATATGTAAGGACTAAAGGATAATGCGCC 140	Db 193 TTAACTCTGTGCTAGCTAACGCTTAAGTATAAGTATGCTGATCTCTCTGCTGATCTCTACTACCTCTGTG 134		
	Qy 1354 -----TTGGCTAACCTGCTATCTCTCTGCTGATCTACTACCTGTGCTG 1404	Qy 1354 -----TTGGCTAACCTGCTATCTCTCTGCTGATCTACTACCTGTGCTG 1404		
	Db 139 AGTCCACTTCGCARATTTTATCAATGTCCTTAATAATTCTCTCTTCTTGTG 80	Db 133 AGTCCACTTCGCAAATAUTTTATCAATGTCCTTAATAATTCTCTCTTGTG 74		
RESULT	3	RESULT	3	
LOCUS	BQ135164/c	LOCUS	BQ135164	
DEFINITION	INIT1.4_B05_g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis mRNA sequence.	DEFINITION	INIT1.4_B05_g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius multifiliis mRNA sequence.	
ACCESSION	BQ135164	ACCESSION	BQ135164	
VERSION	1	VERSION	1	
KEYWORDS		KEYWORDS		
SOURCE		SOURCE		
ORGANISM	Eukaryota: Alveolata: Ciliophora; Oligohymenophorea; Ichthyophthirius multifiliis	ORGANISM	Eukaryota: Alveolata: Ciliophora; Oligohymenophorea; Ichthyophthirius multifiliis	
COMMENT		COMMENT		
REFERENCE	Hymenostomatida; Ophyloglenina; Ichthyophthirius.	REFERENCE	1 (bases 1 to 602)	
AUTHORS	Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.	AUTHORS	Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.	
TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)	TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)	
JOURNAL	Unpublished (2002)	JOURNAL	Unpublished (2002)	
COMMENT	Contact: Cordonnier-Pratt MM	COMMENT	Contact: Cordonnier-Pratt MM	
REFERENCE	Laboratory for Genomics and Bioinformatics	REFERENCE	Laboratory for Genomics and Bioinformatics	
AUTHORS	The University of Georgia, Department of Plant Biology	AUTHORS	The University of Georgia, Department of Plant Biology	
TITLE	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	TITLE	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	
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source 1. .602  
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 /strain="G5"  
 /db\_xref="taxon:5932"  
 /clone\_lib="G5 trophont cDNA (INIT1)"  
 /note="Vector: pBluecript SK(-) from Lambda Zap II;  
 Site\_1: EcoRI; Site\_2: EcoRI; the library was made from  
 trophont polyA+ RNA of the G5 parasite strain.  
 Double-stranded cDNA was linked to EcoRI adaptors, size  
 fractionated, and material >500 bp cloned into lambda ZAP  
 II. Plasmid DNA for sequencing was prepared by mass  
 excision."  
 BASE COUNT 214 a 103 c 92 g 193 t  
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Query Match 3.9%; Score 54.4; DB 14; Length 607;  
 Best Local Similarity 51.7%; Pred. No. 0.0008;  
 Matches 155; Conservative 0; Mismatches 136; Indels 9; Gaps 1;

Qy 1114 GCTACCCGTAGCGTCAGTGGCTCMGAGTGCTGCTGGAACCGTGTGACCGGA 1173  
 Db 381 GCTACCTCACTACAGCAGCTGGCTGCGGTGAGCTGGTAGATGGT 322  
 Qy 1174 ACCACCTCTACCTACAGCAGCTGGCTGAGGTGCTGACTCTCTAC 1233  
 Db 321 ACATCAACTAAATTGTAGCTTACAGTGAATGACTAAAGTTAGCTA 262  
 Qy 1234 ACCACCAAGGACGCCAGGGGACTGGGTGGAATGCACCTGTAACAAAG 1293  
 Db 261 GCATCAAACATCGTGTGAGCTGACTGATCTAAAGG 202  
 Qy 1294 CTGACCTCTGGAGCTGAGCTAACCTGCCAGGCTGAGCTGCTAGTGA 1353  
 Db 201 TTAACTCTGGTGTGCTACAAGTATAGCTGAAAGCTTAATGGCC 101  
 Qy 1354 -----TTCGCTTAACTCCCTGCTATCTACCTACCCCTGCTG 142  
 Db 141 AGTCCACCTTCGAAATTATTCATGTCCTTAATTATTCTATTTGTTG 41

RESULT 5  
 BQ135057/c

LOCUS BQ135057 658 bp mRNA linear EST 22-APR-2002  
 DEFINITION INITI\_1\_F12\_b1\_A006 G5 trophont cDNA (INIT1) Ichthyophthirius  
 multifiliis cDNA, mRNA sequence.  
 ACCESSION BQ135057  
 VERSION BQ135057.1 GI:20261156  
 KEYWORDS EST  
 SOURCE  
 ORGANISM Ichthyophthirius multifiliis.  
 Ichthyophthirius multifiliis.

REFERENCE 1 (bases 1 to 607)  
 AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,  
 Dickerson,H., Lin,T.-L. and Pratt,L.H.  
 TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 Sequences have been trimmed to exclude PolyA, vector, and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20.  
 Seq. primer: JEN REV  
 High quality sequence stop: 67  
 POLYA-No.  
 FEATURES source  
 source 1. .607  
 /organism="Ichthyophthirius multifiliis"





			KEYWORDS	Ichthyophthirius multifiliis.
			SOURCE	Ichthyophthirius multifiliis.
			ORGANISM	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
			REFERENCE	Humenosomatida; Opstryglenina; Ichthyophthirius. 1 (bases 1 to 599)
			AUTHORS	Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,T.-L. and Pratt,L.H.
			TITLE	An EST database for Ichthyophthirius multifiliis (G5 isolate)
			JOURNAL	Unpublished (2002)
			COMMENT	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
b	231	GCTAAATTAGCCGCTATAATGNGCACTCTGTCTGGCACTCTGTGTACAGACGGA	290	
b	1174	ACCACCTTACCTACAGCAGCTGCCTCGGTGAAAGTGTCGACTCTAC 1233		
b	291	GTAACCTCTATACGTACCTCATATGTTAATGTGTTAAAGCTGGCTTAC	350	
RESULT 10				
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DEFINITION		INITI_2-G01.bl-A006 G5 trophont cDNA (INITI) Ichthyophthirius		
ACCESSION		BQ134985		
VERSION		GI:20261084		
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AUTHORS				
TITLE				
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ACCESSION		BQ134821		
VERSION		GI:20261084		
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ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT				

Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: [mpratt@uga.edu](mailto:mpratt@uga.edu)

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq. primer: T7

High quality sequence start: 34

High quality sequence stop: 661

POLYA-No. Location/Qualifiers

1. .661 /organism="Ichthyophthirius multifiliis"  
 /strain="G5"

/db\_xref="taxon:5932"

/clone\_lib="G5 trophont cDNA (INIT1)"

/note="Vector: pBluescript SK(-) from Lambda Zap II;  
 Site\_1: EcoRI; Site\_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.

Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."

BASE COUNT 197 a 124 g 213 t

ORIGIN 216 a 127 g 206 t

Query Match 2.8%; Score 40; DB 14; Length 661;  
 Best Local Similarity 58.3%; Pred. No. 6.9;

LOCUS Matches 70; Conservative 0; Mismatches 0; Gaps 0;

DEFINITION QY 1114 GCTACCCCTGAGTCGCTCAGTGGCTCGGAAACCGTGCTGACCGACCGA 1173

Db 406 GCTAAATTAGCCGCATANTGTGGCACTGAATGICCTGGACTCTGTAAAGCGGA 465

QY 1174 ACCACCTCTACCTACAAAGCAGGCTGCTCTCTGAGTGTGCTAACCTCTAC 1233

Db 466 GTAACACCTATACTGTACTCTCATATAATGTGTAAATGCTGGCTTTAC 525

RESULT 13 BQ135196/c

LOCUS INITI\_4\_E06..91\_A006 G5 mRNA linear EST 22-APR-2002

DEFINITION multiF5l11s CDNA, mRNA sequence.

VERSION BQ135196

KEYWORDS EST.

SOURCE Ichthyophthirius multifiliis.

ORGANISM Hymenostomatida: Alveolata: Ciliophora: Oligohymenophorea;

1. (bases 1 to 65) Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,

Dickerson,H., Lin,T.-L. and Pratt,L.H.

TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)

JOURNAL Unpublished (2002)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: [mpratt@uga.edu](mailto:mpratt@uga.edu)

Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq. primer: T7

High quality sequence start: 42

High quality sequence stop: 675

POLYA-No. Location/Qualifiers

1. .675 /organism="Ichthyophthirius multifiliis"

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/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."
origin 216 a 127 g 206 t

Query Match 2.8%; Score 40; DB 14; Length 675;
Best Local Similarity 58.3%; Pred. No. 7;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1114 GCTACCCCTGAGTCGCTCAGTGGCTCGGAAACCGTGCTGACCGACCGA 1173
Db 377 GCTAAATTAGCCGCATATGTGGCACTGAATGTCCTGGCACTCTGTAAAGCGGA 318

QY 1174 ACCACCTCTACCTACAAAGCAGGCTGCTCTCTGAGTGTGCTAACCTCTAC 1233
Db 317 GTAACACCTATACTGTACTCTCATATAATGTGTAAATGCTGGCTTTAC 258

RESULT 14 AL529709
LOCUS AL529709_LTI_NFL001_NBc4 Homo sapiens cDNA clone CS0DD005YC18_5
DEFINITION prime, mRNA sequence.
ACCESSION AL529709
VERSION AL529709_1 GI:12793202
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contac: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 EVRY cedex - France
Email: segenogenoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES source
  1. .856
  /organism="Homo sapiens"
  /db_xref="taxon:606"
  /clone="CS0DD005YC18"
  /note="Organelle: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Peng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
```

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BASE COUNT 238 a 205 g 161 t 102 others
ORIGIN Query Match 2.8%; Score 40; DB 9; Length 856;
Best Local Similarity 37.2%; Pred. No. 8;
Matches 55; Conservative 34; Mismatches 59; Indels 0; Gaps 0;
QY 7 AACAAACATCCTGGTGAATCTGATCATCTCTGTCATCACACCAGATCAGTCGCTAAC 66
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RESULT 15

BFI91747

LOCUS 239119 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.

DEFINITION 565 bp linear EST 02-NOV-2000

ACCESSION BFI91747

VERSION GI:11075116

KEYWORDS EST,

SOURCE pig

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 555)

AUTHORS Fahrnkrug, S.C., Freking, B.A., Rohrer, G.A., Casas, E., Stone, R.T., Heaton, M.P., Gross, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.

TITLE Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

JOURNAL Unpublished (2000)

COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: smith@email.marc.usda.gov

PCR PRIMERS AGAAACAGCTAATGACCATT

FORWARD: AGAAACAGCTAATGACCATT

BACKWARD: GTTTCGCCATCGACGACG

Plate: 67 row: O column: 16

Seq primer: ATTTGGACACTATAG.

FEATURES Location,Qualifiers

source 1..565

/organism="Sus scrofa"  
<db\_xref=taxon:9833  
<clone lib="MARC 2PIG"  
<tissue\_type="pooled"  
<lab\_host="DH10B"

BASE COUNT 115 a 147 c 161 g 141 t 1 others

ORIGIN

Query Match 2.8%; Score 39.8; DB 12; Length 565;

Best Local Similarity 50.0%; Pred. No. 7.2;

Matches 98; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Db 493

QY 1022 TCGACGGAAACAACTTCAGGTGGATCTTCAGCTGTAAGCTGTCCCTGTAACAGG 1081

Db 313 TCTAGGAAAGATCCCTCGAGAAAATGATCAAGCTTCTGATTAACATGAAGGCCTCTGATAAACATGA 372

QY 1082 TCGGGGGAGCTGGTGGCTACCGCTGGAGAACCGCTACCCCTGATCGCTCAGTGCTCTCG 1141

Db 373 ATAGGGGGGGGGGGGGATGTTGGAGGGGGGGATGTTGGGGGGGGGGGGACCCCCGGGGGGCTGTTCTG 432

QY 1142 AGTGGCCCTGTAACCGTGGTGAACCGTGGTGAACCGAACCCCTACCTACAAGGAGCTGCT 1201

Db 433 TTGTTCTGTTGTCAGGGTTGTCAGGGCAATAACCCCTCACCTTCACCCGGAGT 492

QY 1202 CTGAGCTGTGAAGTG 1217

Db 493 TCCCGTGTGAGCGAGCTG 508

Search completed: February 16, 2003, 22:25:06

Job time : 1454.15 secs